

1600

#2/ Raw Seq.

OIPE

J. string

RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/10/024,396

TIME: 18:06:07

Input Set : A:\RTS-0339 Sequence Listing.txt

Output Set: N:\CRF3\01152002\J024396.raw

RECEIVED
MAR 13 2002
TECH CENTER 1600/2900

ENTERED

3 <110> APPLICANT: Kenneth W. Dobie
5 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF CD36L1 EXPRESSION
7 <130> FILE REFERENCE: RTS-0339
9 <140> CURRENT APPLICATION NUMBER: US/10/024,396
9 <141> CURRENT FILING DATE: 2001-12-18
9 <160> NUMBER OF SEQ ID NOS: 91
12 <210> SEQ ID NO: 1
13 <211> LENGTH: 20
14 <212> TYPE: DNA
15 <213> ORGANISM: Artificial Sequence
17 <220> FEATURE:
19 <223> OTHER INFORMATION: Antisense Oligonucleotide
21 <400> SEQUENCE: 1
22 tccgtcatcg ctcttcaggg 20
25 <210> SEQ ID NO: 2
26 <211> LENGTH: 20
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
32 <223> OTHER INFORMATION: Antisense Oligonucleotide
34 <400> SEQUENCE: 2
35 atgcattctg cccccaagga 20
38 <210> SEQ ID NO: 3
39 <211> LENGTH: 2566
40 <212> TYPE: DNA
41 <213> ORGANISM: Homo sapiens
43 <220> FEATURE:
45 <220> FEATURE:
46 <221> NAME/KEY: CDS
47 <222> LOCATION: (70)...(1599)
49 <400> SEQUENCE: 3
50 cgtcgccgtc cccgtctcct gccaggcgcg gagecctgcg agccgcgggt gggccccagg 60
52 cgcgccagac atg ggc tgc tcc gcc aaa gcg cgc tgg gct gcc ggg gcg ctg 111
53 Met Gly Cys Ser Ala Lys Ala Arg Trp Ala Ala Gly Ala Leu
54 1 5 10
56 ggc gtc gcg ggg cta ctg tgc gct gtg ctg ggc gct gtc atg atc gtg 159
57 Gly Val Ala Gly Leu Leu Cys Ala Val Leu Gly Ala Val Met Ile Val
58 15 20 25 30
60 atg gtg ccg tcg ctg atc aag cag cag gtc ctt aag aac gtg cgc atc 207
61 Met Val Pro Ser Leu Ile Lys Gln Gln Val Leu Lys Asn Val Arg Ile
62 35 40 45
64 gac ccc agt agc ctg tcc ttc aac atg tgg aag gag atc cct atc ccc 255
65 Asp Pro Ser Ser Leu Ser Phe Asn Met Trp Lys Glu Ile Pro Ile Pro
66 50 55 60
68 ttc tat ctg tcc gtc tac ttc ttt gac gtc atg aac ccc agc gag atc 303
69 Phe Tyr Leu Ser Val Tyr Phe Phe Asp Val Met Asn Pro Ser Glu Ile
70 65 70 75

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72	ctg	aag	ggc	gag	aag	ccg	cag	gtg	cgg	gag	cgc	ggg	ccc	tac	gtg	tac	351
73	Leu	Lys	Gly	Glu	Lys	Pro	Gln	Val	Arg	Glu	Arg	Gly	Pro	Tyr	Val	Tyr	
74		80					85					90					
76	agg	gag	tcc	agg	cac	aaa	agc	aac	atc	acc	ttc	aac	aac	aac	gac	acc	399
77	Arg	Glu	Ser	Arg	His	Lys	Ser	Asn	Ile	Thr	Phe	Asn	Asn	Asn	Asp	Thr	
78	95				100					105					110		
80	gtg	tcc	ttc	ctc	gag	tac	cgc	acc	ttc	cag	ttc	cag	ccc	tcc	aag	tcc	447
81	Val	Ser	Phe	Leu	Glu	Tyr	Arg	Thr	Phe	Gln	Phe	Gln	Pro	Ser	Lys	Ser	
82				115						120					125		
84	cac	ggc	tcg	gag	agc	gac	tac	atc	gtc	atg	ccc	aac	atc	ctg	gtc	ttg	495
85	His	Gly	Ser	Glu	Ser	Asp	Tyr	Ile	Val	Met	Pro	Asn	Ile	Leu	Val	Leu	
86			130						135					140			
88	ggt	gcg	gcg	gtg	atg	atg	gag	aat	aag	ccc	atg	acc	ctg	aag	ctc	atc	543
89	Gly	Ala	Ala	Val	Met	Met	Glu	Asn	Lys	Pro	Met	Thr	Leu	Lys	Leu	Ile	
90		145					150					155					
92	atg	acc	ttg	gca	ttc	acc	acc	ctc	ggc	gaa	cgt	gcc	ttc	atg	aac	cgc	591
93	Met	Thr	Leu	Ala	Phe	Thr	Thr	Leu	Gly	Glu	Arg	Ala	Phe	Met	Asn	Arg	
94		160					165					170					
96	act	gtg	ggt	gag	atc	atg	tgg	ggc	tac	aag	gac	ccc	ctt	gtg	aat	ctc	639
97	Thr	Val	Gly	Glu	Ile	Met	Trp	Gly	Tyr	Lys	Asp	Pro	Leu	Val	Asn	Leu	
98	175				180					185				190			
100	atc	aac	aag	tac	ttt	cca	ggc	atg	ttc	ccc	ttc	aag	gac	aag	ttc	gga	687
101	Ile	Asn	Lys	Tyr	Phe	Pro	Gly	Met	Phe	Pro	Phe	Lys	Asp	Lys	Phe	Gly	
102				195						200				205			
104	tta	ttt	gct	gag	ctc	aac	aac	tcc	gac	tct	ggg	ctc	ttc	acg	gtg	ttc	735
105	Leu	Phe	Ala	Glu	Leu	Asn	Asn	Ser	Asp	Ser	Gly	Leu	Phe	Thr	Val	Phe	
106			210						215					220			
108	acg	ggg	gtc	cag	aac	atc	agc	agg	atc	cac	ctc	gtg	gac	aag	tgg	aac	783
109	Thr	Gly	Val	Gln	Asn	Ile	Ser	Arg	Ile	His	Leu	Val	Asp	Lys	Trp	Asn	
110		225					230					235					
112	ggg	ctg	agc	aag	gtt	gac	ttc	tgg	cat	tcc	gat	cag	tgc	aac	atg	atc	831
113	Gly	Leu	Ser	Lys	Val	Asp	Phe	Trp	His	Ser	Asp	Gln	Cys	Asn	Met	Ile	
114		240					245					250					
116	aat	gga	act	tct	ggg	caa	atg	tgg	ccg	ccc	ttc	atg	act	cct	gag	tcc	879
117	Asn	Gly	Thr	Ser	Gly	Gln	Met	Trp	Pro	Pro	Phe	Met	Thr	Pro	Glu	Ser	
118	255				260					265				270			
120	tcg	ctg	gag	ttc	tac	agc	ccg	gag	gcc	tgc	cga	tcc	atg	aag	cta	atg	927
121	Ser	Leu	Glu	Phe	Tyr	Ser	Pro	Glu	Ala	Cys	Arg	Ser	Met	Lys	Leu	Met	
122			275						280					285			
124	tac	aag	gag	tca	ggg	gtg	ttt	gaa	ggc	atc	ccc	acc	tat	cgc	ttc	gtg	975
125	Tyr	Lys	Glu	Ser	Gly	Val	Phe	Glu	Gly	Ile	Pro	Thr	Tyr	Arg	Phe	Val	
126			290						295				300				
128	gct	ccc	aaa	acc	ctg	ttt	gcc	aac	ggg	tcc	atc	tac	cca	ccc	aac	gaa	1023
129	Ala	Pro	Lys	Thr	Leu	Phe	Ala	Asn	Gly	Ser	Ile	Tyr	Pro	Pro	Asn	Glu	
130			305				310					315					
132	ggc	ttc	tgc	ccg	tgc	ctg	gag	tct	gga	att	cag	aac	gtc	agc	acc	tgc	1071
133	Gly	Phe	Cys	Pro	Cys	Leu	Glu	Ser	Gly	Ile	Gln	Asn	Val	Ser	Thr	Cys	
134		320					325					330					
136	agg	ttc	agt	gcc	ccc	ttg	ttt	ctc	tcc	cat	cct	cac	ttc	ctc	aac	gcc	1119

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137 Arg Phe Ser Ala Pro Leu Phe Leu Ser His Pro His Phe Leu Asn Ala
138 335 340 345 350
140 gac ccg gtt ctg gca gaa gcg gtg act ggc ctg cac cct aac cag gag 1167
141 Asp Pro Val Leu Ala Glu Ala Val Thr Gly Leu His Pro Asn Gln Glu
142 355 360 365
144 gca cac tcc ttg ttc ctg gac atc cac ccg gtc acg gga atc ccc atg 1215
145 Ala His Ser Leu Phe Leu Asp Ile His Pro Val Thr Gly Ile Pro Met
146 370 375 380
148 aac tgc tct gtg aaa ctg cag ctg agc ctc tac atg aaa tct gtc gca 1263
149 Asn Cys Ser Val Lys Leu Gln Leu Ser Leu Tyr Met Lys Ser Val Ala
150 385 390 395
152 ggc att gga caa act ggg aag att gag cct gtg gtc ctg ccg ctg ctc 1311
153 Gly Ile Gly Gln Thr Gly Lys Ile Glu Pro Val Val Leu Pro Leu Leu
154 400 405 410
156 tgg ttt gca gag agc ggg gcc atg gag ggg gag act ctt cac aca ttc 1359
157 Trp Phe Ala Glu Ser Gly Ala Met Glu Gly Glu Thr Leu His Thr Phe
158 415 420 425 430
160 tac act cag ctg gtg ttg atg ccc aag gtg atg cac tat gcc cag tac 1407
161 Tyr Thr Gln Leu Val Leu Met Pro Lys Val Met His Tyr Ala Gln Tyr
162 435 440 445
164 gtc ctc ctg gcg ctg ggc tgc gtc ctg ctg ctg gtc cct gtc atc tgc 1455
165 Val Leu Leu Ala Leu Gly Cys Val Leu Leu Leu Val Pro Val Ile Cys
166 450 455 460
168 caa atc cgg agc caa gag aaa tgc tat tta ttt tgg agt agt agt aaa 1503
169 Gln Ile Arg Ser Gln Glu Lys Cys Tyr Leu Phe Trp Ser Ser Ser Lys
170 465 470 475
172 aag ggc tca aag gat aag gag gcc att cag gcc tat tct gaa tcc ctg 1551
173 Lys Gly Ser Lys Asp Lys Glu Ala Ile Gln Ala Tyr Ser Glu Ser Leu
174 480 485 490
176 atg aca tca gct ccc aag ggc tct gtg ctg cag gaa gca aaa ctg tag 1599
177 Met Thr Ser Ala Pro Lys Gly Ser Val Leu Gln Glu Ala Lys Leu
178 495 500 505
180 ggtcctgagg acaccgtgag ccagccaggc ctggccgctg ggccctgaccg gccccccagc 1659
182 ccctacaccc cgcttctccc ggaactctccc agcagacagc cccccagccc cacagcctga 1719
184 gctcccagc tgccatgtgc ctgttgacac cctgcacaca cgccctggca cacatcacaca 1779
186 catgcgtgca ggcttgtgca gacactcagg gatggagctg ctgctgaagg gacttgtagg 1839
188 gagaggctcg tcaacaagca ctgttctgga acctctctc cacgtggccc acaggctgac 1899
190 cacaggggct gtgggtcctg cgtccccttc ctggggtgag cctggcctgt cccgttcagc 1959
192 cgttgggcca ggcttctctc cctccaaggt gaaacactgc agtcccgtg tgggtgctcc 2019
194 ccatgcagga cgggccaggc tgggagtgcc gccttctctg gccaaattca gtggggactc 2079
196 agtgcccagg ccctggcaag agctttggcc ttggtctacc tgccaggcca ggcaaagcgc 2139
198 ctttacacag gctcggaaa acaatggagt gagcacaaga tgccctgtgc agctgcccgga 2199
200 gggctctccg ccaccccggc cggactttga tcccccgaa gtcttcacag gcactgcac 2259
202 ggggtgtctg ggcgcccttt cctccagcct aaactgacat catcctatgg actgagccgg 2319
204 ccactctctg gccgaagtgg cgcaggctgt gcccccgagc tgccccacc ccctcacagg 2379
206 gtccctcaga ttataggtgc ccaggctgag gtgaagaggc ctgggggccc tgccttcagg 2439
208 gcgctcctgg accctggggc aaacctgtga cccttttcta ctggaataga aatgagtttt 2499
210 atcatctttg aaaaataatt cactcttgaa gtaataaacg tttaaaaaaa tggaaaaaaa 2559
212 aaaaaaa 2566

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215 <210> SEQ ID NO: 4
216 <211> LENGTH: 20
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
222 <223> OTHER INFORMATION: PCR Primer
224 <400> SEQUENCE: 4
225 ctgggctctt cacgtgttc 20
228 <210> SEQ ID NO: 5
229 <211> LENGTH: 19
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
235 <223> OTHER INFORMATION: PCR Primer
237 <400> SEQUENCE: 5
238 tcagcccggt ccacttgtc 19
241 <210> SEQ ID NO: 6
242 <211> LENGTH: 26
243 <212> TYPE: DNA
244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
248 <223> OTHER INFORMATION: PCR Probe
250 <400> SEQUENCE: 6
251 ccagaacatc agcaggatcc acctcg 26
254 <210> SEQ ID NO: 7
255 <211> LENGTH: 19
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
261 <223> OTHER INFORMATION: PCR Primer
263 <400> SEQUENCE: 7
264 gaaggtgaag gtcggagtc 19
267 <210> SEQ ID NO: 8
268 <211> LENGTH: 20
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
274 <223> OTHER INFORMATION: PCR Primer
276 <400> SEQUENCE: 8
277 gaagatggtg atgggatttc 20
280 <210> SEQ ID NO: 9
281 <211> LENGTH: 20
282 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
287 <223> OTHER INFORMATION: PCR Probe
289 <400> SEQUENCE: 9
290 caagcttccc gttctcagcc 20
293 <210> SEQ ID NO: 10

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RAW SEQUENCE LISTING

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TIME: 18:06:07

Input Set : A:\RTS-0339 Sequence Listing.txt

Output Set: N:\CRF3\01152002\J024396.raw

294 <211> LENGTH: 972

295 <212> TYPE: DNA

296 <213> ORGANISM: Homo sapiens

298 <220> FEATURE:

300 <400> SEQUENCE: 10

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301 ggcactgcat cgggttgtct ggcgcccttt tcctccagcc taaactgaca tcatectatg 60
302 gactgagccg gccactctct ggccgaagtg gccgcaggct gtgccccga gctgccccca 120
303 cccctcaca gggctccctca gattataggt gccacgctg aggtgaagag gcctgggggc 180
304 cctgccttcc gggcgctcct ggaccctggg gcaaacctgt gaccttttc tactggaata 240
305 gaaatgagtt ttatcatctt tgaataataa ttcactcttg aagtaataaa cgtttaaaaa 300
306 aatgggatgc ctgcctctgt gacagccttg tttgctgagg tcgtgggggt gggggcctct 360
307 gggaagttcc gggctcctct tctcttggtc aatagctcct ttctgggtgg tgccaagagc 420
308 gtctctccca ggccgggctg ctggcttacc ttctgtgttt ttcaaatttc aacctgtgtc 480
309 aatgttgagt ttcatagaaa tactgcatga gtacgccctt gtttagaagc agcagggtct 540
310 gagtcccatc ccacagcccc agtgcagacg cttttgccac ttttgcatgg ggccccctgg 600
311 atgtgtttct gtgcatttat ctacaaatcc tggtgcccg aggacatgcc cgtgtgttct 660
312 aaggcctttg ctctctgtcc ttacctaaaa ggtgagaaga gagcggttta gaggacagat 720
313 gggcatctaa aagtctcatc ttagtgtgat cctgcaacga ggattctcga ttggcatcct 780
314 gctcagttga gctggacatt ccaggattta ggtgcccggt actactggga ggacaggctc 840
315 cgcaattcag atttgaacac ttgggaaggt gcctacaagg gtttcccaa ataagatatt 900
316 taggggatac ccgtcgcaat ttgcaaaagg ggtacgcccc tttgttatgg cgtggactta 960
317 caaagttttc gt 972

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319 <210> SEQ ID NO: 11

320 <211> LENGTH: 719

321 <212> TYPE: DNA

322 <213> ORGANISM: Homo sapiens

324 <220> FEATURE:

326 <400> SEQUENCE: 11

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327 gctcaggccc cgcccctgcc gccggaatcc tgaagcccaa ggtctgcccg ggggcggtcc 60
328 ggcgggcgcc gcatggggc ataaaaccac tggccacctg ccgggctgct cctgcgtgcg 120
329 ctgccgtccc ggatccaccg tgccctctgc gcctgcgtgc ccggagtcct cgccgtgtgc 180
330 gtctctgtcg ccgtccccgt ctccctgccg gcgaggagcc ctgcgagccg cgggtggggc 240
331 ccaggcgccg agacatgggc tgctccgcca aagcgcgctg ggctgccggg gcgctggggc 300
332 tcgcggggct actgtgcgct gtgctggggc ctgtcatgat cgtgatggtg ccgtcgctca 360
333 tcaagcagca ggtccttaag aacgtgcgca tcgacccag tagcctgtcc ttcaacatgt 420
334 ggaaggagat ccctatcccc ttctatctct ccgtctactt ctttgacgtc atgaaccca 480
335 gcgagatcct gaagggcgag aagccgcagg tgcgggagcg cgggccctac gtgtacagg 540
336 cagttcaggc acaaaagcaa catcaccttc aacaacaacg acaccggtgt ccttcctcga 600
337 gtaaccgacc ttccagttcc agccctccaa gtcccacggc tcggaagagc gactaccatc 660
338 gtcattgccc aaatcctggt cttgggtgcg gcggtgatga tggagaataa gcccatgag 719

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341 <210> SEQ ID NO: 12

342 <211> LENGTH: 485

343 <212> TYPE: DNA

344 <213> ORGANISM: Homo sapiens

346 <220> FEATURE:

W--> 348 <221> NAME/KEY: exon:exon junction

349 <222> LOCATION: (277)...(278)

350 <223> OTHER INFORMATION: exon 12:exon 14

352 <400> SEQUENCE: 12

VERIFICATION SUMMARY

DATE: 01/15/2002

PATENT APPLICATION: US/10/024,396

TIME: 18:06:08

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:348 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:379 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:391 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:395 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:407 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13